

**Genetic diversity among some wild populations of lima bean
(*Phaseolus lunatus* L.) proceeding from the Central Valley of Costa Rica**

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In situ conservation is mainly proposed to preserve wild populations and landraces as they could evolve with environment and pest changes (1, 2, 3). To provide further insight for *in situ* conservation of wild population of self compatible species in which varying levels of outcrossing occur, *P. lunatus* has been chosen as a plant model in the framework of a IPGRI project funded by the National Overseas Agency (AGCD) of Belgium. A survey on wild populations of lima bean has been carried out by Dr. O. Rocha and his team (University of Costa Rica, San José) in the Central Valley of Costa Rica, a country located in the Mesoamerican diversity centre (4). Eighteen wild populations proceeding from the 400 ones discovered in the Valley have been evaluated using allozymes to improve knowledge on the organization, distribution and amount of genetic diversity on wild populations of lima bean. These wild populations have been selected for the following criteria: size, altitude, rainfall and geographic distribution inside this Valley.

A preliminary study using 17 isozymes representing 22 loci was made and revealed 10 polymorphic loci. This rate of polymorphism (45%) seems to be similar to the one found among wild populations of *P. vulgaris* (43%) by Koenig and Gepts (1989) (5). Nonetheless in our case only wild populations proceeding from a single region have been evaluated while Koenig and Gepts used wild populations from the entire New World distribution of the common bean. Apparently the polymorphism of lima bean is greater than the one observed in *P. vulgaris*. In order to carry on this study, the following isozymes representing 10 loci have been selected: ADH, CAP, GPI, IDH, MDH, PGDH and PGM because only one tissu (cotyledon) and one buffer (Histidine-citrate) are needed and zymograms are simple (without any inter-loci interactions) to interpret. Table 1 summarizes the data for the 10 loci with their alleles and allelic frequencies in parentheses. Five loci are monomorphic: CAP, IDH, MDH2, PGDH2 and PGM1. Eleven populations possess fixed alleles for all the loci, one population has a single polymorphic locus, 4 populations (E25, E28, S32 and T11) have 2 polymorphic loci and the last 2 populations (KM30 and KM40) show 3 polymorphic loci. The most common allele - allele 100 - is not always the single found in a population. For example the wild population J29 is characterized by the allele *ADH*²⁶¹ while the G20 population has the allele *GPI*⁹⁶. It is not always the most common allele at one locus which is present in the Central valley of Costa Rica. *PGM*²⁸⁵ is more common in the majority of the wild populations (10 populations) except for SR16 a wild population localized in the extreme north limit of the valley and having the allele 100. The two alleles of the MDH1 locus possess a good distribution among the wild populations: seven populations have the allele 140, six show the allele 100 and five populations have the 2 alleles at different frequencies.

These first results on the lima bean wild populations proceeding from a single region have given some promising information about the management of the genetic resources of this species. Usually the wild populations surveyed in the Central Valley are small (<20 plants) and are growing along fences or inside coffee fields. These populations must undergo a significant drop in size during weeding. In spite of this kind of management, the preliminary results show that 50% of the tested loci are polymorphic and 43% of the wild populations possess 2-3 polymorphic loci. The maintenance of this polymorphism among the wild populations could be explained completely or partially by one or more of the following factors: survival of some plants along the fences, seed dormancy and/or allogamy emphasized by the proximity of the wild populations. As suggested by Loveless and Hamrick (1984) (6), fluctuating size of population involves a low genetic variation within population due to drift while seed dormancy and long-lived cycle increase it. These last ecological factors retard loss of alleles, reduce effects of drift and increase the mating opportunities.

Three wild populations (E25, KM40 and S32) have been retained for a more detailed study concerning the genetic structure and the dynamic of natural populations. A fourth population coming from San Ramon (extreme north limit) will be selected due to its lateness in blooming. A study has been also undertaken to assess correlations between the presence or absence of a population and some ecological factors.

Table 1. Allelic frequencies observed among wild populations of *P. lunatus* proceeding from the Central Valley of Costa Rica

	n°	ADH2	CAP	GP11	IDH	MDH1	MDH2	PGDH1	PGDH2	PGM1	PGM2
E25	10	61 (0.35) 100 (0.65)	100	100	100	100 (0.6) 140 (0.4)	100	100	100	100	85
E27	9	100	100	100	100	140	100	100	100	100	85
E28	42	100	100	100	100	100 (0.8) 140 (0.2)	100	86 (0.8) 100 (0.2)	100	100	85
E29	4	100	100	100	100	100	100	100	100	100	
E50	10	100	100	100	100	100	100	100	100	100	85 (0.56) 100 (0.44)
G20	12	100	100	96	100	100	100	100	100	100	85
J29	10	61	100	100	100	140	100	100	100	100	85
KM30	34	61 (0.02) 100 (0.98)	100	96 (0.03) 100 (0.97)	100	100 (0.09) 140 (0.91)	100	100	100	100	85
KM40	39	61 (0.76) 100 (0.24)	100	100	100	100 (0.79) 140 (0.21)	100	100	100	100	85 (0.52) 100 (0.48)
KM57	9	100	100	100	100	100	100	100	100	100	85
P1	10	100	100	100	100	140	100	100	100	100	85
S7	4	100	100	100	100	140	100	100	100	100	85
S27	5	100	100	100		140	100	100	100	100	
S32	15	100	100	96 (0.8) 100 (0.2)	100	140	100	100	100	100	85 (0.8) 100 (0.2)
SR8	10	61	100	100	100	100	100	100	100	100	
SR10	10	100	100	100	100	140	100	100	100	100	
SR16	4	100	100	100	100	100	100	100	100	100	100
T11	6	61 (0.83) 100 (0.17)	100	100	100	100 (0.5) 140 (0.5)	100	100	100	100	85

n°: number of plants evaluated

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